

GenCore version 4.5  
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On protein - protein search, using sw model  
Run on: September 4, 2002, 16:12:45 ; Search time 101.54 seconds  
(without alignments)  
44.770 Million cell updates/sec

Title: US-09-052-089a-2  
Perfect score: 2393  
Sequence: 1 MPILSILCTCSDFDFHSRDV..... VRKTVSSASQPKLDTFLCQ 470  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR71:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	919	38.4	433	T30807 TRAF interacting protein - Fugu rubripes
2	221	9.2	506	2 P85016 probable RING zinc finger protein
3	204.5	8.5	425	T25457 hypothetical protein
4	200.5	8.4	1690	2 T113030 microtubule binding protein
5	192.5	8.0	1325	2 T42722 male-enhanced anti-myosin heavy chain
6	191.5	8.0	2139	T18296 myosin heavy chain
7	190	7.9	2017	1 A36014 myosin II heavy chain
8	190	7.9	2057	2 S61477 chromosome segregation protein
9	186.5	7.8	1156	E59444 chromosome segregation protein
10	186.5	7.8	1940	1 S04090 myosin heavy chain
11	185.5	7.8	1039	2 S18199 myosin heavy chain
12	185.5	7.8	1940	1 A24922 myosin heavy chain
13	185.5	7.8	2116	2 A26655 myosin heavy chain
14	183	7.6	1938	1 A40997 myosin heavy chain
15	182.5	7.6	501	A38650 myosin heavy chain
16	181	7.6	1156	2 B70356 chromosome assembly protein
17	181	7.6	2007	1 A23402 myosin heavy chain
18	180	7.5	1992	1 S02771 myosin heavy chain
19	179.5	7.5	1961	1 A61231 myosin heavy chain
20	179.5	7.5	1976	2 A59252 myosin heavy chain
21	179	7.5	1017	2 PC4035 cell cycle-dependent protein
22	178.5	7.5	1999	1 S21801 myosin heavy chain
23	178	7.4	1790	2 S67593 myosin heavy chain
24	177.5	7.4	1957	2 T38077 myosin heavy chain
25	177	7.4	2168	2 T30171 myosin heavy chain
26	176.5	7.4	1509	1 A127224 myosin heavy chain
27	176.5	7.4	1827	2 T16270 myosin heavy chain
28	176	7.4	389	2 B44972 myosin heavy chain
29	175.5	7.3	1133	2 T22976 myosin heavy chain

### ALIGNMENTS

RESULT	1
T30807	TRAF interacting protein - Fugu rubripes
QY	C; Species: Fugu rubripes C; Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000 C; Accession: T30807 R; Cottage, A.J.; Clark, M.; Hawker, K.; Umania, Y.; Wheeler, D.; Bishop, M.; Elgar, F.; FEBS Lett. 443, 370-374, 1999 A; Title: Three receptor genes for plasminogen related growth factors in the genome of Fugu rubripes A; Reference number: Z20880; MUID:99148833 A; Accession: T30807 A; Status: preliminary; translated from GB/EMBL/DBJ A; Molecule type: DNA A; Residues: 1-433 <COT> A; Cross-references: EMBL:AJ010317; NID:e1355235; PID:e1355237; PIDN:CAA09084.1 C; Genetics: A; Gene: TRIP A; Introns: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 3
Query	38.4%
Match	Score 919; DB 2; Length 433;
Best Local Similarity	40.7%; Pred. No. 1.9e-40;
Matches	191; Conservative 87; Mismatches 117; Indels 74; Gaps 6;
Description	TRAF interacting protein - Fugu rubripes
Db	1 MPILSILCTCSDFDFHSRDV..... VRKTVSSASQPKLDTFLCQ 470
QY	C; Species: Fugu rubripes C; Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000 C; Accession: T30807 R; Cottage, A.J.; Clark, M.; Hawker, K.; Umania, Y.; Wheeler, D.; Bishop, M.; Elgar, F.; FEBS Lett. 443, 370-374, 1999 A; Title: Three receptor genes for plasminogen related growth factors in the genome of Fugu rubripes A; Reference number: Z20880; MUID:99148833 A; Accession: T30807 A; Status: preliminary; translated from GB/EMBL/DBJ A; Molecule type: DNA A; Residues: 1-433 <COT> A; Cross-references: EMBL:AJ010317; NID:e1355235; PID:e1355237; PIDN:CAA09084.1 C; Genetics: A; Gene: TRIP A; Introns: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 3
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Match	Score 919; DB 2; Length 433;
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Matches	191; Conservative 87; Mismatches 117; Indels 74; Gaps 6;
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QY	C; Species: Fugu rubripes C; Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000 C; Accession: T30807 R; Cottage, A.J.; Clark, M.; Hawker, K.; Umania, Y.; Wheeler, D.; Bishop, M.; Elgar, F.; FEBS Lett. 443, 370-374, 1999 A; Title: Three receptor genes for plasminogen related growth factors in the genome of Fugu rubripes A; Reference number: Z20880; MUID:99148833 A; Accession: T30807 A; Status: preliminary; translated from GB/EMBL/DBJ A; Molecule type: DNA A; Residues: 1-433 <COT> A; Cross-references: EMBL:AJ010317; NID:e1355235; PID:e1355237; PIDN:CAA09084.1 C; Genetics: A; Gene: TRIP A; Introns: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 3
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Match	Score 919; DB 2; Length 433;
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Matches	191; Conservative 87; Mismatches 117; Indels 74; Gaps 6;
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Db 724 QIELEKESIEQQLAL----KQNELE-DFQKKQKSESEVHLEQEKAQWQKQDLELVEGES 777  
 Qy 104 IDTLDLTDEERNATIVESQHNLNAKMAEMLCSTLKQMK-FLEOQDQETKQARBEAHLRKCK 162  
 Db 778 LKKLQQQLEBERTGHEKLQALEE-----LKEKEETIKERKEQELQOLQSKSAESEA 830  
 Qy 163 MKYME-QELLIQSQRSEVEEMIRDGMVGQSAVEQALAVCVSKKEVNLKARKATGEL 221  
 Db 831 LKVYQVQBOLOQDQQAASGEE-----GSKTVAKLHDEISOLSKSQABETOSBLSKTESN 883  
 Qy 222 ADDRKDLVSSRSKLK-----TLNTEDQAKLERSAQKDIQSDAOEITSRKKSDP 274  
 Qy 884 LEAKSKQLEANGSLEAAKSKSQQECITKLKSEBETQAAQASSYHIDVESTKQ--- 939  
 Db 275 PGNLPEASATNETVSLVLFESPA-----PVMMNPRLHQ-----PPF 311  
 Qy 940 --LEAAWAKALEVKYAEASRAEASDLQDKYKEITDTLHAELQAERSSSSAHTKLSKF 996  
 Db 312 GDEI-----DLNTFDVWMPPTGSGQHCLPKKLCLEARSHMQ----- 351  
 Db 997 SDREYATGKELTSKAD-----AWSQEMLOREKELOELROQLDSDSOTKLLKACER 1048  
 Qy 352 -----NVKVKVHKVKSPKPSQSLSGQRCGELDEELAGAFLPFLRNALVGKOPN 401  
 Db 1049 KERSEFEETIKNLQEEVTAKTENIELSQTGQTQTLQERL-----ITNAELQHK--- 1099  
 Qy 402 RTTAESRSSTDVTRIGFDGLGGRKFQIOPRD-TTIIIRPVVKSKSKQVKRITVSSAS 460  
 Db 1100 --EKMASEDAOKIA-----DLKLTVEAQVANANISATNAELSTVLEV 1141  
 Qy 461 Q 461  
 Db 1142 Q 1142

RESULT 5

T42722  
 male enhanced antigen-2 - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 11-Jan-2000  
 C;Accession: T42722  
 R;Kondo, M.; Sutou, S.  
 DNA Seq 7, 71-82, 1997  
 A;Title: Cloning and molecular characterization of cDNA encoding a mouse male-enhanced a  
 A;Reference number: Z22242; MVID:97217683  
 A;Accession: T42722  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-1325 <KON>  
 A;Cross-references: EMBL:D78270; NID:d1096175; PID:d1020389; PIDN:BA19612.1  
 A;Experimental source: strain CD-1  
 C;Function:  
 A;Description: supposed to play some role for spermatogenesis  
 C;Keywords: leucine zipper

Query Match 8.0%; Score 191.5; DB 2; Length 2139;  
 Best Local Similarity 22.1%; Pred. No. 0.032; Matches 97; Conservative 83; Mismatches 161; Indels 97; Gaps 16;

Db 66 LAQEENNLDAELKNEELDSVKAQLSQK-----DREKKDSQAIIDLTDLTEERNATV 118  
 Qy 1671 VAQEEEEK----QRIEDEIAELKQLEQERTTAAANEAEKKQAEELDEVKFNUEDVYNQR 1726  
 Db 119 ESL--QNALNKAEMLCSTLKQMKFLEOQDQETKQARBEAHLRKCKMKTMEQTELLQSQ 176  
 Db 1727 EKLVAKNSEDAE-----DSIKEEKALE--DEKEITDDNNKLS-----EEIDSLDRY 1775  
 Qy 177 RSEVEEMIRDGMVGQSAVEQALAVCVSKKEVNLKARKGELAELKKQDVLSSSKL 236  
 Db 1776 NALIDSKDSVSKMKEFQDDELVYTKDAALETEKHNAAETMRMLKG---RLEKEAEVYRL 1831  
 Qy 237 KTNTEDQAKLERSAQKDIQSDAOEITSRKKSDDPGNLEPASATNETVSLVLFESP 296  
 Db 1832 EAQKNNLDLQDQERAKAATKDYRADGEKSKMHNEDDVKQDQDKA----- 1876  
 Qy 297 APVEMNPRLHQPPGDEIDLNTF-----VNTPTQPTSSQHCLPKKLCLE-----R 345  
 Db 1877 -----QDLDADKEDELAELDQKWTLYQKSKVFSRQIE-MOEQDLEKAGR 1924  
 Qy 346 ARSPMNVKVKVHKVKSPKPSQSLSGQRCGELDEELAGAFLPFLRNALVGKOPN 393  
 Db 1925 AOKQKQAYVERKLOQELQENDDFEEYKETADKRINTLSAQK-DDQKBL-----EK 1973  
 Qy 394 VLGKQKPNITAE-----SRSSDWDVIGFDLGGRKFQPRDTTIRPVVKSKAKS 447  
 Db 1974 ERGLQDKSDKEVERGLVVKQEELETKVAEVG--GANVSIKVKAKYAEELITEADAL 2031  
 Qy 448 KQVKRITVSSASOPKL 465  
 Db 2032 KAKMKAEEKAKTSQKLD 2049

Qy 208 YEN-----LKEA---RKATGELADRLKKDLVSSRSRKLKTNTELDOA 246

RESULT 7

A36014 myosin heavy chain, nonmuscle - fruit fly (*Drosophila melanogaster*) R;Ketchum, A.S.; Stewart, C.T.; Stewart, M.; Kiehart, D.P.

N;Contains: myosin ATPase (EC 3.6.1.32) J. Mol. Biol. 255, 98-109, 1996

C;Species: *Drosophila melanogaster* A;Title: Molecular organization and alternative splicing in zipper, the gene that enc

C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 19-Jan-2001 A;Accession: A36014; B36014

C;Accession: A36014; B36014 R;Ketchum, A.S.; Stewart, C.T.; Stewart, M.; Kiehart, D.P.

Proc. Natl. Acad. Sci. U.S.A. 87, 6316-6320, 1990 A;Title: Complete sequence of the *Drosophila* nonmuscle myosin heavy-chain transcript: co

A;Reference number: A36014; MUID:90349606 A;Accession: A36014

A;Status: nucleic acid sequence not shown A;Molecule type: mRNA

A;Residues: 1-2017 <KET> A;Cross-references: GB:M35012

C;Genetics:

A;Gene: FlyBase:zip A;Cross-references: FlyBase:FBgn0005634

C;Superfamily: myosin heavy chain; myosin motor domain homology A;Gene: zip

C;Keywords: actin binding; alternative splicing; ATP; coiled coil; hydrolase; methylated A;Cross-references: EMBL:U35816

F;1-2017/Product: myosin heavy chain, form I #status predicted <MA1> R;Mansfield, S.G.; Al-Shirani, D.Y.; Ketchum, A.S.; Newbern, E.C.; Kiehart, D.P.

F;46-2017/Product: myosin heavy chain, form II #status predicted <MA2> submitted to the EMBL Data Library, September 1995

A;Reference number: S61477; MUID:96144835 A;Accession: S61477

A;Molecule type: DNA A;Residues: 1-2057 <MAN>

A;Cross-references: EMBL:U35816

A;Residues: 1-1908; 'NL' 1911-2057 <MAN> A;Cross-references: EMBL:U35816; NID:91141789; PIDN:AB09049.1; PID:91572481

A;Molecule type: DNA A;Cross-references: EMBL:U35816

A;Cross-references: FlyBase:FBgn0005634 A;Cross-references: FlyBase:FBgn0005634

A;Introns: 10/3; 90/3; 162/3; 215/1; 25/3; 263/3; 303/3; 334/3; 1248/1; 1349/3; 1526 A;Cross-references: EMBL:U35816

C;Superfamily: myosin heavy chain; myosin motor domain homology C;Keywords: alternative splicing; ATP; nucleotide binding; P-Loop F;135-859/Domain: myosin motor domain homology <MMOT> F;225-232/Region: nucleotide-binding motif A (P-loop)

F;596-631/Region: actin binding #status predicted A;Cross-references: EMBL:U35816

F;605-631/Region: actin binding #status predicted <COI> A;Cross-references: EMBL:U35816

F;888-1328/Region: S2 A;Cross-references: EMBL:U35816

F;1329-2017/Region: light meromyosin A;Cross-references: EMBL:U35816

F;221/Binding site: ATP (Lys) #status predicted F;45, 755/Active site: Cys #status predicted

Query Match 7.9%; Score 190; DB 1; Length 2017; Best Local Similarity 23.8%; Pred. No. 0.036; Matches 88; Conservative 61; Mismatches 145; Indels 76; Gaps 14; Query 56 KTINKLFFDLAQEEENVDAE--FLKFLNDSVKAQLSQDRKRDSD-----AI 103 Db 1263 KTVLEK-----AKGTLAENADLATLRSVNSRDRRKQASQIAELQVKLAE 1314

Qy 104 IDTLDLTLER---NATVESLQNALNKAEMLSTLKKMFLQEQDETQKAREAH- 158 Db 1315 IERARSELQEKCTKQLOEAEINTNQOLEELKASAALKSASNHQSOLTEAQOLIEETRQ 1374

Qy 159 --LKCKMMTMEQTELLIQSQRSEVEEMTRDMCVGQSAVEQLAVCYSLKKEYENLKEAR 215 Db 1415 KLGJSSKLRIESEKEALQEQLEEDDEERKRN--ERKLAEVITMQEIKKAAEADLA 1471

Qy 216 KARGLADRLKKDVLSSRSKSLKL--NTELODAKLERSACKD---LOSADQETLSR 268 Db 1472 KELEEGKKRKLNDQKELAQLRQKELAQNDLDRDKSKKKIQSELEDATEELLEORTKYLE 1531

Qy 269 KKSDDPPGNEPASATNTVSLVFESRAPVEMNPRHQPPGDEIDLNTFDVNTPPT 328 Db 1532 KKGK---NFDKLIAEERAKAISEQIAQERTDAERAREAREKTVLVSREBDEAFD----- 1581

Qy 321 KATGELADRLKKDVLSSRSKSLKL--NTELODAKLERSACKD---LOSADQETLSR 268 Db 1582 -----KIEDELENKRKTLONEELDDLANTOCTADKNVHELEKARRAELAELKAQ 1631

Db 1432 KELEEGKKRKLNDQKELAQLRQKELAQNDLDRDKSKKKIQSELEDATEELLEORTKYLE 1491

Qy 269 KKSDDPPGNEPASATNTVSLVFESRAPVEMNPRHQPPGDEIDLNTFDVNTPPT 328 Db 1492 KKQK---NFDKLIAEERAKAISEQIAQERTDAERAREAREKTVLVSREBDEAFD----- 1541

Qy 329 QTSGSQHCLPKKCLERARSPMNVL-----KKVHKVSKP---ESQLS-LGGQ 372 Db 1592 N-EELEDDDL 1599

RESULT 9

E69444 chromosome segregation protein (smcl) homolog - *Archaeoglobus fulgidus* C;Species: *Archaeoglobus fulgidus*

C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 02-Jun-2000 C;Accession: E69444

C;Accession: E69444 C;Accession: E69444 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod .; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C. A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch

A;Reference number: A69250; MUID:98049343 C;Species: *Drosophila melanogaster* C;Date: 19-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 02-Feb-2001

RESULT 8

S61477 myosin II heavy chain, non-muscle - fruit fly (*Drosophila melanogaster*)

A: Accession: S03442  
 A: Molecule type: DNA  
 A: Residues: 855-1390, 'KK', 1393-1940 <KAR>  
 A: Cross-references: EMBL:Y15695; NID:936504; PIDN:CAA33731.1; PID:91335313  
 R: Steckman, H.H.; Eller, M.; Julian, E.H.; Fertels, S.H.; Sarkar, S.; Sylvester, J.E.;  
 J. Biol. Chem. 265, 3568-3575, 1990  
 A: Title: The human embryonic myosin heavy chain. Complete primary structure reveals e  
 A: Reference number: A35082; MUID:90150423  
 A: Contents: annotation; chromosomal assignment  
 R: Bober, E.  
 A: Reference number: S12458  
 A: Accession: S12460  
 A: Molecule type: mRNA  
 A: Residues: 855-1330, 'G', 1332-1390, 'KK', 1393-1607, 'RA', 1610-1940 <BOB>  
 A: Cross-references: EMBL:Y15193; NID:929463; PIDN:CAA35942.1; PID:929464  
 A: Experimental source: clone gHMHC-E  
 R: Bober, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goedde, H.W.; Arnold, H.H.  
 Eur. J. Biochem. 189, 55-65, 1990  
 A: Title: Identification of three developmentally controlled isoforms of human myosin  
 A: Reference number: S09331; MUID:90235862  
 A: Accession: S09333  
 A: Molecule type: mRNA  
 A: Residues: 856-901, 'X', 903-971, 'X', 973-1041, 'X', 1043-1111, 'X', 1113-1181, 'X', 1183-125  
 1, 'X', 1673-1741, 'X', 1743-1811, 'X', 1813-1881, 'X', 1883-1940 <BOB>  
 A: cross-references: EMBL:XS1593  
 C: Genetics:  
 A: Gene: GDB:MYH3  
 A: cross-references: GDB:119443; OMIM:160720  
 A: Map position: 17p13.1-p13.1  
 C: Superfamily: myosin heavy chain; myosin motor domain homology  
 C: Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle  
 F: 89-1767/Domain: myosin motor domain homology <MMOT>  
 F: 179-186/Region: nucleotide-binding motif A (P-loop)  
 F: 549-586/Region: actin binding #status predicted  
 F: 656-678/Region: actin binding #status predicted  
 F: 840-1940/Region: coiled coil #status predicted  
 F: 840-1280/Region: S2  
 F: 1281-1940/Region: light meromyosin  
 F: 130/modified site: N6, N6,N6-trimethyllysine (Lys) #status predicted  
 F: 185/Binding site: ATP (Lys) #status predicted  
 F: 696,706/Active site: Cys #status predicted

Query Match 7.8%; Score 186.5; DB 1; Length 1940;  
 Best Local Similarity 20.3%; Pred. No. 0.052; Gaps 7;  
 Matches 77; Conservative 83; Mismatches 177; Indels 43; Gaps 7;  
 QY 54 GKTIIINKLFFDQLAQEENVY-LDAEFLKNEEDSVKQLSQDREKRDQSAQIDTIRDTLE 112  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1262 GKNNEIIGRSLSLTOKRSRQLEAGELSRQLEKEVTSVQLSRSKQAFTOOTEELKROL 1321  
 QY 113 ERNATVESLQLNAINKAEMLCSTIJKKOMKKFLEROQDETQKAREEH----RICKMKT 166  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1322 EENKAKNLAHQSSRHDQJLREQEEDEQGKELQARLKSANSEVAQPRKTFDAI 1381  
 QY 167 EOEJLLQSQRSVEEMIRDMGVQSAVEQLAVYCVSLK-----EYENLKEARKATG 219  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1382 ORTEELEPQQ---EKLQARLQDSEEQEVAVNAKACASLEKTKIKRQLOGEVEDLMDVERAN 1437  
 QY 220 ELADRLKQDLSRSRKLTNTEDQAKLERSAQKQDQASQELTSRKISDDPGNL 279  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1438 SLLAALDKKQRNEDKDVLAEKWTKCEESQAELEASLKEBSRSLSTELFLKLNAYEALDOL 1497  
 QY 280 PASATNEVWSRLVFESPAVPEMINPRLHQPPFGDETLNLTTFDWNTPPTQTSGSQHCLPK 339  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1498 TVKRENKILQEJFADLQEQLAENGKTHE-----LENSRKOLEK 1538  
 QY 340 --KLCLLERRARSMDMVNLKVKHVKVSKPESQISLGGORCVELDEELAGAFLPLFIRNAVLG 396  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1539 ADIQOLALEBEEAALHEEAKLURIOELTQVSEIDRKIAKDEEIQQLKNVQRTV-- 1595

QY 397 OKOPNRITTAESISSTDVYRI 416

Db 1596 : ||| : :: : 1596 ETMOSALDAEVRSRNEAIRL 1615 R;Strehler, E.E.; Mahdavi, V.; Periasamy, M.; Nadal-Ginard, B. C;Species: Gallus gallus (chicken) J. Biol. Chem. 260, 468-471, 1985 C;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 02-Feb-2001 A;Title: Intron position is conserved in the 5' end region of myosin heavy-chain gene C;Accession: S18199 A;Reference number: A22538; MUID:85080119 A;Accession: A22538 A;Molecule type: DNA A;Status: preliminary A;Residues: 1-1039 <ST> A;Cross-references: EMBL:X59552; NID:62995; PIDN:CAA42130.1; PID:962996 A;Note: in the authors' translation 45-Lys is shown after residue 40, and, consequently, C;Superfamily: myosin heavy chain; myosin motor domain homology C;Keywords: ATP; nucleotide binding; P-loop C;402-409/Region: nucleotide-binding motif A (P-loop)

Query Match 7.8%; Score 185.5; DB 2; Length 1039; Best Local Similarity 20.2%; Pred. No. 0.029; Matches 77; Conservative 82; Mismatches 167; Indels 55; Gaps 10; Qy 59 INKLUFFDIAQEENNVL-DAEFLKNEELDSVKAQLSQDKREKRSQASQIIDLTRLEERNA 116 Db 369 MTRLMNDLTQTKTKLQSENGEFVR-QLEEKESLISQLSRCKTSFTQQIBELRQLLEETK 427 Qy 117 TVEISNLNAKEMCSTLKKMFLQDQDTEKQAREAHRLCKMKMTEQFELLIQS 176 Db 428 SKNLAHLAQAAQRIDCDLIREQYEEQEAKEALQRALSRGNAEVQWRKTYEDAIQRE 487 Qy 177 RSE-VEEMRDGMVGQSAVEQALAVCVSLKKYKENLK-----EARKATGELADRK 226 Db 488 ELEDAKKKLLARIQAEAAIEAAANAKCSSLKAKHRLQNEQEDMIDLEKANAAASIDK 547 Qy 227 KDLVSSRSKLTLM---TELDQAKLELRSQAQKQDOSADEEITSURKSDDPPNLEPASA 283. Db 548 K---QRGDFKINDWKQYEEQESQAEASQKEARSLSTLEFLKLNAYEETLHLETIKR 603 Qy 284 TNETVSLRUFESPAPVEMPRHOPPGEDEIDNTFDVNTPTGTSQSOHCLP 343 Db 604 ENKNEQEESIDLTMQISEGKNLH-----EIE-----KVKQVEQENSEVQL 647 Qy 344 ERASRPMQVNLKVKVSKPESQLSLGGORCVGSELDEELAGAFPLFIRNAVLGQKQPNT 403 Db 648 EEEAGALEHEEESKTLRFQELSLQKADFERKLAKDEEMQNT-----RRNQQT 696 Qy 404 -----TAERSSTDVIRI 416 Db 697 IDSLQSTLDSEARSNEAIRL 717

RESULT 12

A21922 myosin heavy chain, skeletal muscle, embryonic - rat R;Strehler, E.E.; Streicher-Page, M.A.; Perriard, J.C.; Perriamy, M.; Nadal-Ginard, B. A;Title: Complete nucleotide and encoded amino acid sequence of a mammalian myosin heavy C;Species: Rattus norvegicus (Norway rat) C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 19-Jan-2001 C;Accession: A21922; MUID:87060988 A;Accession: A24922 A;Molecule type: DNA A;Residues: 1-1940 <STR> A;Cross-references: GB:X04267; GB:X05004; NID:956658; PIDN:CAA27817.1; PID:91619328

RESULT 13

A26655 myosin heavy chain [similarity] - slime mold (Dictyostelium discoideum) N;Contains: myosin ATPase (BC 3.6.1.32) C;Species: Dictyostelium discoideum

A; Accession: A26655; MUID:87092266	C; Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 02-Feb-2001
A; Residues: 1-2116 <W2R>	A; Accession: A24728
A; Cross-references: GB: M14628; GB: M11938; NID: 9167834; PIDN: AAA33227.1; PID: 9167835	A; Molecule type: mRNA
A; Title: Conserved protein domains in a myosin heavy chain gene from Dictyostelium discoideum	A; Residues: 1-1938 <W2R>
A; Reference number: A26655; MUID:87092266	A; Cross-references: GB: X55714; NID: 95611; PIDN: CAA39247.1; PID: 95612
A; Molecule type: DNA	A; Superfamily: myosin heavy chain; myosin motor domain homology
A; Residues: 1-1839	C; Keywords: actin binding; myosin motor domain homology <MM00>
A; Cross-references: GB: M14628; GB: M11938; NID: 9167834; PIDN: AAA33227.1; PID: 9167835	F; 176-1839/Region: nucleotide-binding motif A (P-loop)
A; Title: Phosphorylation of threonine residues on cloned fragments of the Dictyostelium discoideum	F; 547-586/Region: actin binding #status predicted
A; Reference number: A26655; MUID:87092266	F; 655-675/Region: actin binding #status predicted
A; Molecule type: mRNA	F; 835-1938/Region: coiled coil #status predicted <COI>
A; Residues: 2035-2116 <DEL>	F; 835-1276/Region: S2
R; Wagle, G.; Nogel, A.; Scheel, J.; Gerisch, G.	F; 1277-1938/Region: light meromyosin
RBS Lett. 227, 71-75, 1988	F; 182/Binding site: ATP (Lys) #status predicted
A; Title: The rod domain is highly periodic, containing a pattern of 7-residue repeats	F; 693,703/Active site: Cys #status predicted
A; Reference number: S00250; MUID:88112226	
A; Molecule type: DNA	
A; Residues: 1-1839 <WAG>	
C; Comment: The rod domain is highly periodic, containing a pattern of 7-residue repeats	
C; Superfamily: myosin heavy chain; myosin motor domain homology	
C; Keywords: actin binding; ATP; coiled coil; hydrolase; nucleotide binding; P-loop; phosphatase; actin binding; ATP; coiled coil; hydrolase; nucleotide binding; P-loop; phosphatase	
F; 1-818/Domain: globular head <HE>	
F; 89-747/Region: nucleotide-binding motif A (P-loop)	
F; 1819-2116/Domain: alpha-helical rod <ROD>	
Query Match 7.6%; Score 183; DB 1; Length 1938; Best Local Similarity 23.0%; Pred. No. 0.079; Matches 102; Conservative 67; Mismatches 128; Indels 146; Gaps 20; Matches 82; Conservative 60; Mismatches 108; Indels 77; Gaps 15; Gaps 20;	
Qy 55 KKTINKLFFD-----LAQEEENVLDAEFLKINELDSVKAQL-----SQ 92	
Db 903 EKLIMOKADERSQIKLERLDEELQADLEAGLEGKKMMEALNANLKKDILENTIQKAE 962	
Qy 93 KDRKEKRSQADITD-----RTDLEERN-ATVESLQ-----INALINKA 128	
Db 963 QDKAHNDQ-ISTILOGEISQODEHIGKLNNKEKALEEANKKTSDSLQAEEDKCHNLK- 1019	
Qy 129 EMLCSTLKKMFKLEQRDQEIKQAREEARIKCKMK---TMEQIELLOSQRSEVEEM 183	
Db 1020 --LKAKEQALDELENDLEREKKVGDVEKAKKRKGQDLSKSTQENYEDLERVKR-ELEEN 1076	
Qy 184 IR-----DMGVGQSAVEQAVYCVSILKKEVYENLKEARKATGELADRLKKDVLSS 232	
Db 1077 VRRKAEISSLNSKLEDEQNLVSQLQRKIKELQARIEELEELAERNARAKVKEKORAE 1136	
Qy 233 RSKLQKLTNLELDQ-----KLSLRSQAKDLOSA---DQELTSRKSKSDDP 274	
Db 1137 NREELELGERLDEAGGATSAQELINKKREAEILKTRDLEEASLQHQAQISALRKHHQD- 1195	
Qy 275 PGNLEPASATNETVSLVFPESAPVEMMNPRHLQPPGDEIDLTTFDVNTPPTGSQ 334	
Db 1196 -----AANEMADQY-----DQLQKVSKLEK---DKDLKREND---DLSQMT 1233	
Qy 335 HCLPKKLCLEARSPRMONVLKVKVSKPESOLS-----LGQRCVGEELDBELAGAFPL 388	
Db 1234 HNMKNKGCEK-----VMQKF-----ESOMSLNARLEDSQRSINEL----- 1270	
Qy 389 FIRNAVILGQKOPNRTAERSST 411	
Db 1271 -----QSOKSRLOAENSDLT 1285	
Qy 295 SPAPVEMMNPRHLQPPGDEIDLTTFDVNTPPTGSQHCLPKKLCIERSAPMNVL 354	
Db 1059 A-----ANKKIQ---GEYTTELNEKF--NSEVYARSN-----WEKSRTKTESQL 1096	
Qy 355 KKVKVSKPESQLSQLGGCGVGEELDEE 381	
Db 1097 VAVN-----NELDEE 1106	
RESULT 14	RESULT 15
A0097 myosin heavy chain, striated adductor muscle - scallop (Aequipecten irradians)	A38650 myosin heavy chain, embryonic smooth muscle - rabbit (fragment)
N; Contains: myosin ATPase (EC 3.6.1.32)	C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Species: Aequipecten irradians	C; Date: 21-Feb-1992 #sequence_revision 21-Feb-1992 #text_change 20-Jun-2000
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001	C; Accession: A38650
C; Accession: A40997; S1357	R; Kuro-o, M.; Nagai, R.; Nakahara, K.; Katoh, H.; Tsai, R.C.; Tsuchimochi, H.; Yazaki, J. Biol. Chem. 266, 3768-3773, 1991
R; Nyitrai, L.; Goodwin, E.B.; Szent-Gyorgyi, A.G.	A; Reference number: A38650; MUID: 91139672
J. Biol. Chem. 266, 18469-18476, 1991	A; Status: Preliminary
A; Title: Complete primary structure of a scallop striated muscle myosin heavy chain. Sequence number: A40997; MUID: 92011595	A; Molecule type: mRNA
A; Reference number: A40997; MUID: 92011595	A; Residues: 1-1501 <KUR>
A; Cross-references: GB:D10280; GB:D90237; NID: 9217729; PIDN: BAA01124.1; PID: 9217730	A; Title: cDNA cloning of a myosin heavy chain isoform in embryonic smooth muscle and
C; Superfamily: myosin heavy chain; myosin motor domain homology	C; Keywords: ATP; smooth muscle

Query Match 7.6%; Score 182.5; DB 2; Length 501;  
Best Local Similarity 22.0%; Pred. No. 0.018; No. of Mismatches 76; Conservative Matches 78; Mismatches 141; Indels 51; Gaps 9;

Qy 68 QEEENVLDLAEFLKNEFLWVKAQLSQDKREKRSQALID--TURDTLEERNATIVE 119  
Db 30 QNKOLRADMEDLIMSKDVGKVNHELESKR-----TLEQVEEMRTQLEELDEDQAL 127

Qy 128 AEMLCSTLKKOMFKQLEQRODE-----TKQREAHRLKCKM-----TMEQIEL 171  
Db 90 LEVNTQAMKAQFEDLQARDEQSEBEKKRLTKQVRELEALEDERKORALAVASKKMEI 149

Qy 172 LLQSQSEVEEMTRDMGIGOSAIEPOLAVYCISLKEYENLKERKATGELADLUKLIVS 231  
Db 150 DLKOLEAQEAAK---ARERRYKVLQRLLQAOQMKDQYRELEAARSBDFIAOSKE--- 202

Qy 232 SRSKLTNTLEDOAKLERSAQKLSQDQEITSRLRKSDDEPPGPNLEPASATNETVSRL 291  
Db 203 SEKKUKSLSAEILOLQEEELASSERARRHAEQEREL---ADELANSASGSKSALLDEKRL 259

Qy 292 ---VFSQAPVEMNPRLHQPPFGDEIDLNTTFDVTNPPTQSGSCHLKP-- 339

Db 260 EAMRQLEEELEQESQNSMELLNDRFK-----TTLQVLTNLNAELAERSAAQSD 309

Qy 340 --KICLLEKRSRSPMQNVLKVKHVKSKPESOLSLGG-QRGVGEELREL 382  
Db 310 NARQOLERONDKIKAQLOELEGAVSKFKATISALEAKIGOLEBQL 355

RESULT 16

B70356 chromosome assembly protein homolog - *Aquifex aeolicus*

C;Species: *Aquifex aeolicus*  
C;Accession: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 02-Jun-2000  
C;Accession: B70356; Warren, P.V.; Gaasterland, T.; Young, W.G.; Denox, A.L.; Graham, D.B.; Ov R;Beckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Denox, A.L.; Graham, D.B.; Ov V;Nature 392, 353-358, 1998  
A;Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.  
A;Reference number: A70300; MUID:98196666  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-1156 <AQF>  
A;Cross-references: GB:AE000699; NID:9298328; PID: AAC06839.1; PID:92983243; GB:AE000655  
A;Experimental source: strain VF5  
C;Genetics:  
A;Gene: xcpC  
C;Superfamily: chromosome segregation protein Smc1

Query Match 7.6%; Score 181; DB 2; Length 1156;  
Best Local Similarity 20.1%; Pred. No. 0.055; No. of Mismatches 81; Conservative Matches 81; Mismatches 92; Indels 88; Gaps 16;

Qy 66 LAGEEENV---LDAEFLKNEFLWVKAQLSQDKREKRSQALID--TURDTLEERNATIVE 119  
Db 207 LKEKEKELEKFLKELRIKRETEA-KILLEKEKEKLERERILNELLSSRLSDEDITQIO 265

Qy 120 SLONALNKAEMLGSTLKKOM-----KFLEQRQDETQKQAREFAHRUKCKMKTMEQTEL 171  
Db 266 ENKELNERLKEVNEKIMPKEVKCFATLLENERSIKKEREKESERVKLEE 325

Qy 172 LLQSQSEVEEMTRDMGIGOSAIEPOLAVYCISLKEYENLKERKATGELADLUKLIVS 231  
Db 326 LINNLILSKENLREVGTLQEELEK-----LKEEYSLKEV----- 361

Qy 232 SRSKLTNTLEDOAKL---ELLSAQKQDQSAQEQEITSRLRKSDDEPPGPNLEPASATN-- 285  
Db 362 ERKLRELEEEERLKEITDEVKLEEKEKLTENKLNSLNKEQEL--EIORANKNIE 419

Qy 286 --ETVSLVLFESPAPV-----EMNIRLHQPPFGDEIDL-NTFDVTNPPTQSGS 335  
Db 390 LEVNTQAMKAQFEDLQARDEQSEBEKKRLTKQVRELEALEDERKORALAVASKKMEI 149

RESULT 17

B43402 myosin heavy chain-B, neuronal - chicken  
C;Contains: myosin ATPase (EC 3.6.1.32)  
C;Species: Gallus gallus (chicken)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 19-Jan-2001  
C;Accession: B43402; A43402  
R;Takahashi, M.; Kawamoto, S.; Adelstein, R.S.  
J. Biol. Chem. 267, 17664-17671, 1992  
A;Title: Evidence for inserted sequences in the head region of nonmuscle myosin specific  
A;Reference number: A43402; MUID:92388144  
A;Accession: B43402  
A;Molecule type: mRNA  
A;Residues: 1-2007 <TAK>  
A;Cross-references: GB:NM93676; NID:9212448; PID:AAA48988.1; PID:9212452  
A;Note: the sequence of residues 212-221 and 632-652 and the corresponding nucleotide  
A;Accession: A43402  
A;Molecule type: mRNA  
A;Cross-references: GB:NM93676; NID:9212448; PID:AAA48985.1; PID:9212449  
C;Comment: Alternatively spliced segments 1 and 2 are found exclusively in nonmuscle  
C;Superfamily: myosin heavy chain; myosin motor domain homology  
C;Keywords: actin binding; alternative splicing; ATP; coiled coil; hydrolase; myosin  
F;1-2007/Product: myosin heavy chain-B, neuronal #status predicted <MYN>  
F;1-211-222-631-653-2007/Product: myosin heavy chain-B, nonmuscle #status predicted <  
F;88-802/Domain: myosin motor domain homology <MYD0>  
F;178-185/Region: nucleotide-binding motif A (P-loop)  
F;212-221/Region: alternatively spliced segment 1 #status experimental  
F;59-593/Region: actin binding #status predicted  
F;632-652/Region: alternatively spliced segment 2 #status experimental  
F;692-714/Region: actin binding #status predicted  
F;875-2007/Domain: coiled coil #status predicted <COL>  
F;1316-1317/Region: S2  
F;1316-2007/Region: light meromyosin  
F;29/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted  
F;732,742/Active site: Cys #status predicted  
F;1954/Binding site: phosphate (Thr) (covalent) #status predicted  
F;1987/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 7.6%; Score 181; DB 1; Length 2007;  
Best Local Similarity 21.5%; Pred. No. 0.1; No. of Mismatches 96; Conservative Matches 96; Mismatches 167; Indels 96; Gaps 16;

Qy 68 QEEENVLDLAEFLKNEFLWVKAQLSQDKREKRSQALID--TURDTLEERNATIVE 119  
Db 1536 QNKOLRADMEDLIMSKDVGKVNHELESKR-----TLEQVEEMRTQLEELDEDQAL 1588

Qy 128 AEMLCSTLKKOMFKQLEQRODETKQAREFAHRUKCKMKTMEQIELLLIQS 179  
Db 1589 TEDAKLRLVNMQAMKAQFEDLQARDEQEEKRLMVKQVRELEALEDERKORALAVA 1648

Qy 180 ---VEEMTRDMGIGO-----SAVEPOLAVYCISLKEYENLKERKATGELADLUKLIVS 226  
Db 1649 AKKRMEDMLKDL-EQQLEANKARDEAKLRLQAOQMKDQYRELEAARRASDEIFQSK 1707

Qy 227 KDLVSSRKKLTNTLEDOAKLERSAQKLSQDQEITSRLRKSDDEPPGPNLEPASATN 286  
Db 1708 E---SERKLKGLEAEILOLQEEFAASERRHAEQEREL--ADELANSASGSKSALLD 1760



A; Residues: 182-218 <BEM>  
 A; Cross-references: GB:L29141; NID:9457249; PIDN:AAA20904.1; PID:9531134  
 C; Genetics:  
 A; Gene: GDB:MYH9  
 A; Cross-references: GDB:120216; OMIM:160775  
 A; Map position: 22q12.3-22q13.1  
 C; Superfamily: myosin heavy chain; myosin motor domain homology  
 C; Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleotide  
 F; 84-174-764-/Domain: myosin motor domain homology <MM0>  
 F; 174-181-/Region: nucleotide-binding motif A (P-1-loop)  
 F; 552-565-/Region: actin binding #status predicted  
 F; 828-837-1938-/Domain: actin binding  
 F; 837-1938-/Domain: coiled coil #status predicted <COI>  
 F; 127-1277-/Domain: S2 #status predicted <DS2>  
 F; 127-1277-/Domain: light meromyosin #status predicted <LMM>  
 F; 1939-1961-/Domain: carboxyl-terminal <CBT>  
 F; 125-1280-/Modified site: N6,N6-trimethyllysine (Lys) #status predicted  
 F; 125-1280-/Binding site: ATP (Lys) #status predicted  
 F; 694-704-/Active site: Cys #status predicted

Query Match 7.5%; Score 179.5; DB 1; Length 1961;  
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 A; Residues: 116-116, 'N', 117-117, 'D', 118-118, 'E', 119-119, 'D', 120-120, 'E', 121-121, 'D', 122-122, 'E', 123-123, 'D', 124-124, 'E', 125-125, 'D', 126-126, 'E', 127-127, 'D', 128-128, 'E', 129-129, 'D', 130-130, 'E', 131-131, 'D', 132-132, 'E', 133-133, 'D', 134-134, 'E', 135-135, 'D', 136-136, 'E', 137-137, 'D', 138-138, 'E', 139-139, 'D', 140-140, 'E', 141-141, 'D', 142-142, 'E', 143-143, 'D', 144-144, 'E', 145-145, 'D', 146-146, 'E', 147-147, 'D', 148-148, 'E', 149-149, 'D', 150-150, 'E', 151-151, 'D', 152-152, 'E', 153-153, 'D', 154-154, 'E', 155-155, 'D', 156-156, 'E', 157-157, 'D', 158-158, 'E', 159-159, 'D', 160-160, 'E', 161-161, 'D', 162-162, 'E', 163-163, 'D', 164-164, 'E', 165-165, 'D', 166-166, 'E', 167-167, 'D', 168-168, 'E', 169-169, 'D', 170-170, 'E', 171-171, 'D', 172-172, 'E', 173-173, 'D', 174-174, 'E', 175-175, 'D', 176-176, 'E', 177-177, 'D', 178-178, 'E', 179-179, 'D', 180-180, 'E', 181-181, 'D', 182-182, 'E', 183-183, 'D', 184-184, 'E', 185-185, 'D', 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PC4035  
cell-cycle-dependent 350k nuclear protein - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 08-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 21-Jul-2000  
C;Accession: PC4035  
R;Li, Y.; Ke, Y.; Kapp, J.A.; Ferrig, N.; Medsger Jr., T.A.; Joshi, H.C.  
Biochem. Biophys. Res. Commun. 212, 220-228, 1995  
A;Title: A novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal domain sufficient for binding to the CDNA encoding a neuronal myosin heavy chain from mammalian brain  
A;Reference number: S21801; MVID:922358;56  
A;Accession: S21801  
A;Molecule type: mRNA  
A;Residues: 1-199 <SUN>  
A;Cross-references: EMBL:X62659  
R;Sun, W.; Chantler, P.D.  
Biochem. Biophys. Res. Commun. 175, 244-249, 1991  
A;Title: A unique cellular myosin II exhibiting differential expression in the cerebral

A;Reference number: PN0013; MVID:91151356  
A;Accession: PN0013  
A;Molecule type: mRNA  
A;Residues: 194-198, 'I' <S0J2>  
A;Experimental source: brain  
C;Superfamily: myosin heavy chain; myosin motor domain homology  
C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleo  
C;Key: F84-763/Region: myosin motor domain homology <MM07>  
C;Key: F174-175/Region: nucleotide-binding motif A (P-loop)  
C;Key: F541-575/Region: actin binding #status predicted  
F;653-675/Region: actin binding #status predicted  
F;836-1999/Region: coiled coil #status predicted <COI>  
F;1277-1999/Region: light meromyosin  
F;180/Modified site: ATP (Lys) #status Predicted  
F;693-703/Active site: Cys #status Predicted  
F;1943/Binding site: phosphate (Ser) (covalent) #status predicted  
F;1943/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 7.5%; Score 179; DB 2; Length 1017;  
Best Local Similarity 21.6%; Pred. No. 0.061; Matches 86; Conservative 69; Mismatches 159; Indels 84; Gaps 9;

QY 56 KTIINKLFFDLAQEEN---VLDPEFLKNEELDSVKAQSLQKDRKDSQATDPLRDTL 111  
Db 56 KDKVVENLERLQLMSRQENQELVILDKRNSKAEVETKQTEEMARSLKVFELDLVIRSEK 115

QY 112 EERNATIVESQNLANKAEMCSTLKKMFLQEQ----- 146  
Db 116 ENLTKQIQEKGQISELDKLISFSKQSOLEKEAQDIOKEESKTAVEMLQNQKLNEAV 175

QY 147 -----DETKQAREBAAHRLCKCKMKTMEQFELLOSQSR----- 179  
Db 176 AACCDQEIMKATEQSLDPRTEEHLNRNIEKARLARHEDKQLCVQQLKSEHHAD 235

QY 180 ---VEEMTRDMGYGOSAVEQLAVCVSCKTKEVNLKEARKATGELADRLKDIVSSRS 234  
Db 236 LLKGKVNLRELEARTNQHEAALNEANSKGKEVTLKAKIEGMQSRLGELDVNTIRS 295

QY 235 KLTNTLTELDDQ---AKLRL--RSAQKDQSDADEITSLRKSDDPPGNL----- 278  
Db 296 EKDLDLNELOKEQERISELBNINSSPFENILQKEQEVQKVMKESSTAMEMLQTLQKSSMR 355

QY 279 --EPASATNTVSIRVVFESPAVEMNPRHQPPFG-DEIDLN--TFDVTNTPQTQSG 332  
Db 356 EWQPCMTKIPVPSAQNLSQSOVTELEKAQOLQGLDEAKNKNYTVLOSSVNGLQEVED 415

QY 333 SQHCLPKK-LCLERARSPMNVLKVKVHKVSKPESOISL 369  
Db 416 GKQKLEKDEEISRLKNQIODOEQOLVSKLSQVEGEHQI 453

RESULT 22  
S21801  
myosin heavy chain, neuronal [similarity] - rat  
N;Alternate names: myosin II  
N;Species: Rattus norvegicus (Norway rat)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 19-Jan-2001  
C;Accession: S21801; PN0013; S18134  
C;Species: Rattus norvegicus (Norway rat)  
C;Accession: S21801; MVID:922358;56  
A;Accession: S21801  
A;Molecule type: mRNA  
A;Residues: 1-199 <SUN>  
A;Cross-references: EMBL:X62659  
R;Sun, W.; Chantler, P.D.  
Biochem. Biophys. Res. Commun. 175, 244-249, 1991  
A;Title: A unique cellular myosin II exhibiting differential expression in the cerebral

A;Reference number: PN0013; MVID:91151356  
A;Accession: PN0013  
A;Molecule type: mRNA  
A;Residues: 194-198, 'I' <S0J2>  
A;Experimental source: brain  
C;Superfamily: myosin heavy chain; myosin motor domain homology  
C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleo  
C;Key: F84-763/Region: myosin motor domain homology <MM07>  
C;Key: F174-175/Region: nucleotide-binding motif A (P-loop)  
C;Key: F541-575/Region: actin binding #status predicted  
F;653-675/Region: actin binding #status predicted  
F;836-1999/Region: coiled coil #status predicted <COI>  
F;1277-1999/Region: light meromyosin  
F;180/Modified site: ATP (Lys) #status Predicted  
F;693-703/Active site: Cys #status Predicted  
F;1943/Binding site: phosphate (Ser) (covalent) #status predicted  
F;1943/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 7.5%; Score 178.5; DB 1; Length 1999;  
Best Local Similarity 20.9%; Pred. No. 0.14; Matches 93; Conservative 81; Mismatches 153; Indels 117; Gaps 15;

QY 48 QCRIQVKGKTIINKLFFDLAQEEN-----LDAEF--LKNLSDVKAQSL 93  
Db 1072 ELKMKOLAKE--EEQLQALRVEERAQKWMALKKIRELQSOSELQEDLESERRSRNA 1129

QY 94 DREKRDQAITLTDLTDLTERRNATIVESQNLANKAEMCSTLKK-----QMKFLQ 144  
Db 1130 EKOKRDLGEELEALKTELDEDLTDSTAQDQLRSKREQEWNILKTKLEEAQTHAQIOEM 1189

QY 145 RQDERQAREBAAHRL--KOKMKT-----QIELLQOS-----QRSZV 180  
Db 1190 ROKHSQAVEAQLAEQLEQFQHQLKAKOTLNERGELANEVKVLLQGRDSEHKRV 1249

QY 181 EEMIRDMG---GOSAVEQLAVCVSCKTKEVNLKEARKATGELADRLKDVSSRL 236  
Db 1250 EAQLOQVNFNEGERRVTLADKVKLQVLDNTVGLSQSDSKSKITKDFSALESQI 1309

QY 237 K-----TNTLTELDAKLELRSQAQDQSAQD-----ITSL 267  
Db 1310 QDTQELLQENRQKLSLSTKLQVDEKNSFREQLEEEEEAKHNLKQJATLHAQVADM 1369

QY 268 RKKSDDPPGNELEPASATN-----ETVSLVLFESPA--PVEMNPRHQPPFCDEIDL 317  
Db 1370 KKKMDSVQGLETAEVVKLQKDLLEGQSRHEEKAQYDKEKVKTRQOELDILLYV 1429

QY 318 N-----TFDVTNTPQTQSGHOSCHPKKLCIERTARSPMNVLKVKVHKVSKPE 364  
Db 1430 DHQRSACALEKKQKFD----QLLAEBITKSAVYDKEKVKTRQOELDILLYV 1483

QY 365 SQLSLLGGQRC-----VGLDEEL 382  
Db 1484 AELEAMEQKAEFLRKNLQEMTERL 1507

RESULT 23  
S67593  
transport protein us01 - yeast (Saccharomyces cerevisiae)  
N;Alternate names: protein D252; protein YDL058w  
C;Species: Saccharomyces cerevisiae  
C;Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 21-Jul-2000  
C;Accession: S67593; A38455; S30782  
R;Bloemberger, H.; Brandst, P.  
submitted to the Protein Sequence Database, July 1996  
A;Reference number: S67593  
A;Accession: S67593  
A;Molecule type: DNA  
A;Residues: 1-1790 <BL0>  
A;Cross-references: EMBL:Z74106; NID:91431058; PID:e253003; PID:91431059; MIPS:YDL058  
A;Experimental source: strain S288C

R; Nakajima, H.; Hirata, A.; Ogawa, Y.; Yonehara, T.; Yoda, K.; Yamasaki, M.  
 J. Cell Biol. 113, 245-260, 1991

A; Title: A cytoskeleton-related gene, *us01*, is required for intracellular protein transport

A; Reference number: A38455; MUID:91185402

A; Accession: A38455  
 A; Residues: 1-189, 'T', 392-724, 'S', 726-1790 <NAK>  
 A; Cross-references: GB:X4378; NID:94777; PIDN:CAA38253.1; PID:94778  
 A; Note: the authors translated the codon ACT for residue 768 as Tle  
 R; Hostetter, M.K.; Herman, D.J.; Bendel, C.M.; McClellan, M.; Tao, N.; Kendrick, K.E.  
 submitted to the EMBL Data Library, February 1993

A; Description: An integrin analogue in *Saccharomyces cerevisiae*.  
 A; Reference number: S30782  
 A; Accession: S30782  
 A; Molecular type: DNA  
 A; Residues: 71-846, 'E', 848-923, 'K', 925-1252, 'I', 1254-1318, 'V', 1320-1460, 'S', 1462-1580, 'S'  
 A; Cross-references: EMBL:103188  
 C; Genetics:

A; Gene: SGD:US01; INV1  
 A; Cross-references: SGD:S0002316; MIPS:YDL059w  
 A; Map position: 4L  
 C; Keywords: coiled coil; transmembrane protein

F; 326-342/Domain: transmembrane #status predicted <TM1>  
 F; 394-410/Domain: transmembrane #status predicted <TM2>  
 F; 617-633/Domain: transmembrane #status predicted <TM3>

Query Match 7.4%; Score 178; DB 2; Length 1790;  
 Best Local Similarity 18.1%; Pred. No. 0.13; Matches 81; Conservative 110; Mismatches 177; Indels 80; Gaps 13; Matches 81; Conservative 110; Mismatches 177; Indels 80; Gaps 13;

Qy 56 KTTINKLFFLDAQEEVNLDA-EFLKNE---LDSVKAQLSQDKREKRSQAIIDTLRDT 110  
 Db 965 KSLANN-YKDMQAEENESLIRKVEEVESKNESSIQLSNIQNQKIDSMEKENFOIERSIEKN 1023

Qy 111 LERNAVATESLQNA---LNKAEMLGSTLKKQMKLQEOREDETKOAREE-AHKCKMKT 165  
 Db 1024 IEQQLKTTISDLEQTKEELISKDSSKDEYESQISLKEKLETATPANDENVNKISLTKT 1083

Qy 166 MEOIETLLOQSRSEVEEIMRDGMGVQOSAVQAVLAVCVSLSKKEYENLKEARKATGELADRL 225  
 Db 1084 REELERELAAYKLNKNELEKLEKSEKALKE-----VRENEELIKEEKIQLEKETAT 1136

Qy 226 KKDVLVSSRSKLUKTNLFDQAKLERSAQK-----DLOSAQDEITSL 267  
 Db 1137 KQQLNLSRNLANLESLEKEHEDELAQQLKRYEQBQANKERQYNEETISOLNDEITSTQOENEST 1196

Qy 268 RKSDDPPGKLEPASATNEYEVSLVLFESPAVPEVMNPRLHQPPGDEIDLNTIDVNTPTQSG 327  
 Db 1197 KKKNDNLEGEVKAMKTSSEBQSNL---KKSIEDAINLQIKE----- 1234

Qy 328 TOTSGSQHCLPKKCLER--SPMVKVVKVSKPESQSLGGQRCVYGEDELALAGA 385  
 Db 1235 -----LKKNETNEASLLESKSVSESETVKKELQDECCNF-KEKEVSELEDKLKS 1284

Qy 386 FPLFIRNAVIGOKOPNRRTAESRSSTDWVIRGFDLGGRKFQPRDTTIRPVYVKSK- 444  
 Db 1285 EDKNSKYLEL-QKESEKIKEELDARTTELKIQLEKINTLNSKAKERSESELSRLKTSSEE 1343

Qy 445 -----AKSKQKRKTVSSAOPKL 464  
 Db 1344 RKNABEQEQLKLNEIQKNOFAFEKERKL 1371

RESULT 25

Query Match 7.4%; Score 177; DB 2; Length 2168;  
 Best Local Similarity 21.3%; Pred. No. 0.18; Matches 105; Conservative 83; Mismatches 174; Indels 130; Gaps 21; Matches 105; Conservative 83; Mismatches 174; Indels 130; Gaps 21;

RESULT 24

Query Match 7.4%; Score 177; DB 2; Length 1957;  
 Best Local Similarity 20.6%; Pred. No. 0.15; Matches 74; Conservative 70; Mismatches 135; Indels 81; Gaps 9; Matches 74; Conservative 70; Mismatches 135; Indels 81; Gaps 9;

Qy 70 EENVLADEAFKNUEDSVKAQLSQDKREKRSQAIIDTLRDTLERNATNESLQNLNAE 129  
 Db 1386 EDNQLATNKKVKNQDNLHNEQIRLKEVKKERESLTSLSLNRQKKSLLQDUA 1445

Qy 130 -MLCSTLKKOMKFLEROQ-----DETOKAREEHRKCKMKTMEQIELLOLQSOSREVE 181  
 Db 1446 HMLDDTSRKNSSLMKTIESINSLSDKSFELASAVEVKALQKHSSESISLMENITSQDQ 1505

Qy 182 EMIRDQMGVQGOSAVEQDQAVCVSLKKEYEN-----LKEARKATG 219  
 Db 1506 BAKERIQVDESTIQELDHETASKNNYEGKLNDKSIIRDSENIEQNLNLAAEKSVA 1565

Qy 220 ELADRKKKDVKVSSRSKLUKTL-----NTLDQAKLELSAOKDQSQADQEIITSRKKD 272  
 Db 1566 RLISTERKESEIIQFNRALDIEYHQSQVESELSGRSLKLTSTEEQALANERLSLTTML 1625

Qy 273 DPPGNELEPASATNETEVSLVLFESPAVPEVMNPRLHQPPGDEIDLNTIDVNTPTQSG 332  
 Db 1626 DLQNGYKDLNNDKLSLE-----DLRTLHSLE-DSVASSL 1658

Qy 333 SQHCLPKKCLERASPMQWNLKKVH-----KVSKEQESOLSGGQRCVGEDELALAG 384  
 Db 1659 QKECKIKSTV-----SLOQVLTSTVQARNAELEDEVRSVSDKIRRDDRC-----EHLSG 1709

QY	158	RLKCKMKMDEQIELLOLSSORSEVEEMIR--DMVGQGOSAVEQAVCVSKKVE-----	209
Db	1686	RIKLOQTHMVEQENQLLKDDELERLQLHRCRPLDSLQKQNSVSVSYNEKLIKKEVLSSEL	1745
QY	210	-----NUKEARKATGELADRLKKDLVSSRSRSLKLTNTEDOAKLER	251
Db	1746	KSCADKLAESSLEHRTATMKGQQTAWEEQESLSKQAVLQVQDLEVLQVNQMA	1805
QY	252	SAQKDLQ-----SADQBITSLRK-----SDPQGNLPEASATNETVS-----	289
Db	1806	EIESDLQTRQEKEAVKQEVMSLHQRLQNAIDKDVNSETAP-HLSGLRQORRISLWDKID	1864
QY	290	REVFESPAPEMANPRLHQPPGDEIDLNIT-----FDVNTPTT-QTSGSQHCLPKKL	341
Db	1865	HLMNEEPOLQICQESKRLQTVQVQNTQADLTHSREKVROLESNLNPLTPKQHQLNQPCTVKS-	1923
QY	342	CLEARSPMQNVIKVKHVKSKPESQLSGQRCVGELDELAGFPLFTRNAVIGQK-Q	399
Db	1924	-TQEQKLTKRECEQSQEQSPT-----RKGQMSLGERLETIHENEGLKKQAO	1975
QY	400	PNRHTAESRSST 411	
Db	1976	PLSTVTPRSPPS 1987	
RESULT	26		
A27224		myosin heavy chain II - Acanthamoeba castellanii	
Nr:contains		myosin ATPase (EC 3.6.1.32)	
C;Species		Acanthamoeba castellanii	
C;Date		31-Dec-1993	#sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C;Accession		A27224	
R;Hammer III, J.A.; Bowers, B.; Paterson, B.M.; Korn, E.D.			
J;Cell Biol 105, 913-925; 1987			
A;Title		Complete nucleotide sequence and deduced polypeptide sequence of a nonmuscle my	
A;Reference number		A27224; NUID:87308395	
A;Accession		A27224	
A;Molecule type		DNA	
A;Cross-references		GB:Y00624; GB:M12702; GB:M12703; GB:M19549; NID:95585; PIDN:CAA68663	
C;Genetics			
A;Introms		69/3; 119/3; 181/2	
C;Superfamily		myosin heavy chain; myosin motor domain homology	
C;Keywords		actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleotide	
F;182-775/Domain		myosin motor domain homology <MMOT>	
F;182-775/Region		nucleotide-binding motif A (P-loop)	
F;544-576/Region		actin binding #status predicted	
F;660-692/Region		actin binding #status predicted	
F;848-1227/Domain		coiled coil #status predicted <COI>	
F;1228-1247/Domain		hinge <HN>	
F;1248-1482/Domain		coiled coil #status predicted <CO2>	
F;1483-1509/Domain		carboxyl-terminal <CBT>	
F;133/Modifited site		N6,N6,N6-trimethyllysine (Lys) #status predicted	
F;188/Binding site		ATP (Lys) #status predicted	
Query Match	7.4%	Score 176.5; DB 1; Length 1509;	
Best Local Similarity	24.5%	Pred. No. 0.13; 113; Indels 73; Gaps 15;	
Matches	81	Conservative 63; Mismatches 113; Indels 73; Gaps 15;	
RESULT	28		
QY	66	LAQEEENVIDAEFKNEKLDVKAQLSQKDRSQASQIDTLRDTLEERMA---TVESL	121
Db	888	LAEE-----DADKLEKDLAALKLKLIDGEKAD-----LEENQALLKKVAGL	931
QY	122	QNALNKAEMLCSTLKKQMFPLQROQDETQKQAREEAEHLKCKMKMTEQIELLOLSSORSEVE	181
Db	932	EELQEQETSAASNDLIEOKRKLAEKGELAKSLEER--NRKALQEAQTKVSEBNELQ	988
QY	182	EMTRDMGVQOSAVFQALVVCVSLKKEYEL-KEARKATGELAD--RLKDVSSRSRSLKT	238
Db	988	DKYDEAAAH-----SLKKEEDLSRELTETKALADENIST--RSKLN	1035
QY	239	-----LNTELDQ--AKELRSQAKDLSQADETSLRKSDDPGPNLIPASATNETV	288
Db	1036	TERGADDVRNELDVYATKLOLEKTKSL--EELAQTROLEEKGKRAASRAKOL	1092
QY	289	SRLVFESPAPEMMRNLRHQPPGDEIDLNNTFDVWTPPRTSGSQHCLPKLKCLRARS	348
Db	1093	GOQLEDARSEVDSLKSRLS---AAERSLKTAKDQRDLDQGQ-----LIEDERT	1136
QY	349	PMONVLUKKVH---KVKSPKESQL-SIGGOR	373
Db	1137	VRANVQKQKALFALKJTELEQDQVTAQDQK	1166
RESULT	27		
Db	116270	hypothetical protein F35D11.11 - Caenorhabditis elegans	
C;Species		Caenorhabditis elegans	
C;Date		20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999	
C;Accession		T6270	
R;Fulton, B.		Submitted to the EMBL Data Library, June 1995	
A;Description		The sequence of C. elegans cosmid F35D11.	
A;Reference number		218487	
A;Accession		T6270	
A;Status		preliminary; translated from GB/EMBL/DBJ	
A;Molecule type		DNA	
A;Residues		1-1827 <FULL>	
A;Cross-references		EMBL:U29381; NID:9868214; PID:9868224; PIDN:AAA68757.1; CESP:F35D11.11	
A;Experimental source		strain Bristol N2	
A;Introns		76/2; 131/3; 159/3; 185/3; 221/3; 253/3; 320/1; 869/3; 1133/3; 1205/2; 12	
C;Genetics			
Query	Match	7.4%	Score 176.5; DB 2; Length 1827;
Best	Local Similarity	25.3%	Pred. No. 0.16; 61; Mismatches 63; Indels 35; Gaps 9;
Matches	61	Conservative 63; Mismatches 82; Indels 35; Gaps 9;	
QY	52	QVGKTT-----INKLFFDLAQEEENVLD-----AEFLKNELDVSKAQLSOKDRKKD	99
Db	657	QVNERTRQISEANEKIDDAARKNDALLEDDVATWQEKYEQKLMEEEMRRGQEKEREAD	716
QY	100	SQAIIDPLR-----DTLEERNATVESLQNAINKAEMCSCPLKQK-MFLEQRQDFTQ	151
Db	717	LRALDDLRGNFDKLNLKQVTVDSLINEI-----SSLKEQLNKSEKEELLR	769
QY	152	AREEAFHLKCKMKTMEQIEL-LIQSQRSVEEMIRDMGVQOSAVEQAVCVSKKVE	210
Db	770	MEELEQKNEAEKMEKEYVQLQLAEDQGQVNFKEC--EARMNELTKIHMLMEHQ	826
QY	211	IKEARKATGELADRLKKDLVSSRSRSLKLTNTEDOAKLERSAQKDLQSADE-TSLRK	269
Db	827	IKVQDHLTTEEVERLKERM--RKELERLNEONDGDRAEWSNERRLESSKNEAVTELQE	883
QY	270	K 270	
Db	884	R 884	
RESULT	28		
B44972		paramyosin - nematode (Onchocerca volvulus) (fragments)	
C;Species		Onchocerca volvulus	
C;Date		14-May-1993 #sequence_revision 14-May-1993 #text_change 02-Jul-1998	
C;Accession		B44972	
R;Limberger, R.J.; McReynolds, L.A.			
Mol. Biochem. Parasitol. 38, 271-280, 1990			
Title		Filarial paramyosin: cDNA sequences from Dirofilaria immitis and Onchocerca	
A;Reference number		A44972; MUID:90220759	
A;Accession		B44972	
A;Status		preliminary	
A;Molecule type		RNA	

A; Residues: 1-389 <LIM>  
 A; Cross-references: GB:429734; GB:M29735; GB:M29736; GB:M29737; GB:M29738; GB:M29739; GE  
 C; Superfamily: myosin heavy chain; myosin motor domain homology

Query Match 7.4%; Score 176; DB 2; Length 389;  
 Best Local Similarity 21.9%; Pred. No. 0.029; Mismatches 140; Indels 84; Gaps 15;  
 Matches 87; Conservative

Qy 65 DLAAEDEENVYDAAEFLNEKQKQLSOKSDREKDSOAITDTLDTLEERNATESLONA 124  
 Db 27 DQLQDKHKAERKAERELQHQVKQLAQOLEEAR----RRLDAERTS---QLQHQ 76

Qy 125 LNAEMLCSTLKKQMKFLQEQDTEKQAREEAKHLCKRMKTMQECIELLQ--SQ---- 176  
 Db 77 LHQVQLELDLSVVKYALHHEVEDLRRK----MLQKAEYEBOIEJEMLOKISQLEAKS 130

Qy 177 --RSEVEEMIRDMGVGOSAVEQALAVYCVSILKEVENEENLICKARTKAGTVELGELADRKLK---DLV 230  
 Db 131 RLQEVLEVLVLDL--EKLAR----ENKKLQDHLHEAKA---LADANRKHEDLE 178

Qy 231 SSR--SKLKLNTLELDQAKLLERSA-----OKDQOSADETSLSRK 270

Db 179 NARLAGEIRELRLQALKESRARRDODENRAQRALAEQOQRIEMMERRLOQKEEERALKRN 238

Qy 271 SDDPPGNLNPASARNET----VSLVFEPPAVPMMPRLHQPPFGDBIDLWTFDNT 325  
 Db 239 MQFEDTRLTAALEDAEARMAKELAQLKKYQAEIAELEMV----DNLNQLAGSLEDTO 292

Qy 326 PPTQTSGSQHCKLPKKLCLERSPQMVNLKKVHKVSKPESQSLISGGRCVGELD 379

Qy 380 EELAGAFPLFLIRNAQKOPNRTTAESRSSTDVRI 416

Db 353 TRIRD---LEALDEEPRRRKETAGKNSASKIYV 384

RESULT 29  
 T22976 hypothetical protein F59A2.6 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Accession: T22976; T23157  
 R;Lightning, J.  
 submitted to the EMBL Data Library, June 1994  
 A;Accession: T22976  
 A;Status: preliminary; translated from GB/EMBL/DBDJ  
 A;Residues: 1-1133 <WIL>  
 A;Cross-references: EMBL:Z34801; PIDN:CAA84332.1; GSPDB:GN00021; CESP:F59A2.6

R;Burton, J.  
 submitted to the EMBL Data Library, October 1995  
 A;Reference number: Z17700  
 A;Accession: T23157  
 A;Status: preliminary;  
 A;Molecule type: DNA  
 A;Residues: 1-1133 <WIL>  
 A;Cross-references: EMBL:Z66514; PIDN:CAA91344.1; GSPDB:GN00021; CESP:F59A2.6

A;Gene: CESP:F59A2.6  
 A;Name: CESP:F59A2.6  
 A;Intros: 13/2; 43/3; 107/3; 413/3; 492/3; 567/3; 635/3; 710/3; 738/3; 795/2; 1008/3; 1

Query Match 7.3%; Score 175.5; DB 2; Length 1133;  
 Best Local Similarity 20.4%; Pred. No. 0.1; Mismatches 92; Conservative 108; Mismatches 154; Indels 97; Gaps 22;

Qy 68 QEPENVLDAE--FLKNELDLSVKAQLSQDRKRS-QAIIITLRTDLE----RNAT 117

Db 93 EESKVKLSEKQAFENEKEQEREEQLAKAMEKINSEQILDEVTKLLEQSEEELAARGA 152  
 Qy 118 VESQNALKAAEMCSTLKKQMFQLEQDTEKQAREE-----AHLRKCKMKTMEQ 168  
 Db 153 IQELTEKLESEKETSTAALEVKSKKDSSENLSKPSMTEAMKTKQULNCEKQDEA 212

Qy 169 IELLSQSRSEVEEMIRDMGVGQ----SAVEOLAVYCVSILKEVENEENLICKARTKAGTVELGELADRKLK---DLV 220  
 Db 213 VELIKQ-KEEVERKNMDSDEVQKOLLESTTSEMVKHAAEATVKQ--LEPAQS--- 265

Qy 221 LADRKKDVSRSRKLKT----NTELDQAKLERSAQKQDQSADEETSLRKSDQPP 275

Db 266 -IENLKKDADENR-LKTALESDESSAISEITKOMEAKKELBASERKEKSELREQD-- 320

Qy 276 GNLPAP-SATNEVTSRLFEEPPAVPM----NPRLHOPPGDEDTLNTTFDVNTPP 327

Db 321 -RLQKVNHGQDIOKL--OKTWELMAMRIAKSTDEKLAEROLAGEL-E-NAKEDLV 376

Qy 328 TQTSGSQHCKLPKKLCLERSPQMVNLKKVHKVSKPESQSLISGGRCVGELD 375  
 Db 377 EE-----KHKGIORQAGALDAEKEV-KVLIQELEQSALESQELASSOKADK 426

Qy 376 GELDEELACAGFPFLIRNAVLGQKOPNRTTAESRSSTDVRI--IGFDGIGRKFQIRD 432  
 Db 427 QELKEKL-----QHQKRSSELETAENMRSLTATLENSINSETEILKOL 472

Qy 433 TTIRPVPVSKAKS--KOKVRIKTVSSAQ 461

Db 473 ETIDKELQARQQTPEKALTEBEINVNTLSIIEK 503

RESULT 30  
 S04027  
 parmyosin - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Accession: 04-Dec-1992 #sequence revision 04-Dec-1992 #text\_change 24-Nov-1999  
 R;Kagawa, H.; Gengyo, K.; McEachan, A. D.; Brenner, S.; Karn, J.  
 J. Mol. Biol. 207, 311-333, 1989  
 A;Title: Parmyosin gene (unc-15) of *Caenorhabditis elegans*. Molecular cloning, nucleic acid sequence, and expression pattern  
 A;Reference number: S04027; MUID:89320026  
 A;Accession: S04027  
 A;Molecule type: DNA  
 A;Residues: 1-866 <KAG>  
 A;Cross-references: EMBL:X08068  
 R;Karn, J.  
 submitted to the EMBL Data Library, June 1988  
 A;Reference number: S05282  
 A;Accession: S05282  
 A;Molecule type: DNA  
 A;Residues: 'MERLISLEPMELMERLQELLLIVSLESK', 13-866 <KAR>  
 A;Cross-references: EMBL:X00668  
 R;Schrifter, L.A.; Waterston, R.H.  
 J. Mol. Biol. 207, 451-454, 1989  
 A;Title: Phosphorylation of the N-terminal region of *Caenorhabditis elegans* parmyosin  
 A;Reference number: S04470; MUID:89329036  
 A;Accession: S04470  
 A;Molecule type: protein  
 A;Residues: 2-41; 143-167; 195-216; 299-318; 787-802; 807-836 <SCH>  
 A;Note: the amino end of the mature protein is blocked  
 A;Note: the composition of a 32P-labeled peptide containing residues 2-13 was determined  
 C;Genetics:  
 A;Gene: unc-15  
 A;Intros: 29/3; 55/3; 74/3; 103/3; 140/3; 159/2; 232/3; 267/3; 578/2; 621/3  
 C;Superfamily: myosin heavy chain; myosin motor domain homology  
 C;Keywords: acetylated amino end; coiled coil; phosphoprotein  
 F;2/Modifed site: acetylated amino end (Ser) (in mature form) #status predicted  
 F;6,8,14,16/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 7.3%; Score 175; DB 2; Length 866;  
 Best Local Similarity 21.8%; Pred. No. 0.081;



RESULT 33

F96673 hypothetical protein F1011.30 [Imported] - *Arabidopsis thaliana* (mouse-ear cress)

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

Db 443 F96673 FIRNAVLGKQPNRRTAERSSTWVRFGFGGRTRKTIQPRTTIIRPVPKSAKS 447

Db 496 LIIKAAEQSEVRNRAVEELK-----RSGISGYG-----TLELIRVKDEMYS 538

RESULT 33

F96673 hypothetical protein F1011.30 [Imported] - *Arabidopsis thaliana* (mouse-ear cress)

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Cai, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yiu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A;Reference number: A86141; MUID:21016719

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1313 <STO>

A;Cross-references: GB:AE005173; NID:95042434; PIDN:AD38273.1; GSPDB:GN00141

C;Genetics: F1011.30

A;Map position: 1

Query Match 7.3%; Score 175; DB 2; Length 1313; Best Local Similarity 21.9%; Pred. No. 0.13; Matches 100; Conservative 81; Mismatches 126; Indels 150; Gaps 20; QY 67 AQESEENVLD---AEFLNKLDSVKAQL---SQDREKRQSQALDTDLRQLEERNATES 120

Db 182 AEATKIAEIAHAAEKAELLAELGRKLALGSKKEKEALEGNEIVSKL-----SEIEL 234

QY 121 LQNLANKAEMCLSTLKKQMFLEQDREKQAR-----EEA 156

Db 235 LRGELEKVILESSILKEOGLVIEQLVQDLEAAKMAESCTNNSYEEWKVVKHLEKEVEES 294

QY 157 HRLKCK-----MKTW-----EQTELL---LQSQRSEWEEMIRD 187

Db 295 NRSKSSASSESMESVYMKQLAELNHVLHETKSDNAQEKEKIELKTIEAQRTDLEEYQCV 354

QY 188 GVGOSAVEOFLAVCVSLKKEYE-----NLKEARKATGEGLAD----- 223

Db 355 CIAKEEASKLLENVESIKSELEISQEEKTRALNEKAATSNIONLLDORTESIELERCK 414

QY 224 ---RLKDLVSSRSKLUKLNTEDQAKLRLRAQKDQASDODBITSLRKSDPPGNE 279

Db 415 VEEKSKKDMESTHLALQBASTHSSEAKATLQCQEELKNCESQVDISKASRE----- 468

QY 280 PASATNETVSLRFESPAPVEMMNPRLHOPPFDEID-LNTTD-----VNMPPTOTSGS0HC 336

Db 469 ---TNEKVEKMLEA-----KNEIDSLKSTVDIONEFENSKGWEQ- 507

QY 337 LPKKL---CLERAR-----SPMONVLKVKH--VSKESQSLGQGQCVGE--- 377

Db 508 --KELHLMGCVKVKSEEEENSSSQEVSLVNLKESEEDACARREEASLKNKNVVAEGEV 565

QY 378 --DEEL--AGAPLFLIRNAVLGKQPNRNTTRESR 409

Db 566 KYQETLGEAKAESMMLKESLLDKEEDLKNTBEISS 602

RESULT 34

I52300 giantin - human

N;Alternate names: qcp372

C;Species: *Homo sapiens* (man)

C;Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 20-Aug-1999

R;Sohd, M.; Misumi, Y.; Fujiwara, T.; Nishioka, M.; Ichihara, Y.

Biochem. Biophys. Res. Commun. 205, 1399-1408, 1994

A;Title: Molecular cloning and sequence analysis of a human 372-kDa protein localized to the endoplasmic reticulum membrane

A;Reference number: I52300; MUID:95100974

A;Accession: I52300

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 1-3225 <RES>

A;Cross-references: GB:D25542; NID:9662389; PIDN:BA05025.1; PID:908869

C;Superfamily: giantin

Query Match 7.3%; Score 174.5; DB 2; Length 3225; Best Local Similarity 21.1%; Pred. No. 0.39; Matches 115; Conservative 88; Mismatches 174; Indels 169; Gaps 20; QY 30 HLCQLIQWE-----TAPSRTCPQCRCIOVGGKTIINKLFFDIAQEEENVLD----- 76

Db 686 NLNQNLIEEKKKNADNNSSAFTALSEERIQLLSQVKELSWMTLERAQVKOLEMLAEERQ 745

QY 77 -----EFLKNEEDSVKAQLSQDKRBRKDSQAI 103

Db 746 RRLDYESQTADHNLTEQIHSLSIEAKSKDVKEIQLVNLQEDDVOLQSEQSFLRISQ 805

QY 104 IDTLR-DTE-ER---NATVPSLONALKNA-----LGSTLQKMKLEQDDET 149

Db 806 LQNESEVLEEGAEVRHTSKVLSQSKQLEITKMDQLEKKERDVTIQLQTEEK 865

QY 150 K-----QAREEAHLRKCRMKT-EQIELLQOSORSEVEEMIRDGV----- 189

Db 866 DQOVTETISFSMTERKVKVOLNEEKFGLVQVTKTEOLNLSSRAEAKKEQVEEDNEVSSG 925

QY 190 -----GQSAVEQLAVYCIVSLKKEVNLKEA-----RKATGELADRKKDVLSS 232

Db 926 KQNYDEMSPAQQTISKEELQHEFDLKKENQRRKQALINRKELQVRSLEELANL 985

QY 233 RSKIKT-----LNTEDQAKLRLSAQD 256

Db 986 KDSKKEIPLSETERGEVENEEDKENKEYSEKCVTSKCOBIEIVLQTISEKEVQLHQI 1045

QY 257 LQ---SADQEIITSRKSSDDPPONLERASATNETVSLRFESPAPVEMMNPRLHQPPFG 313

Db 1046 LEELKAAEBOFOALVKQNNQ---TLQDKUNQDILQLQAEISENOAIQKLITSNTDASGD 1102

QY 314 EIDINTTDFVNTPTQTSGSQHQLP---KKLCLERARSPMONVLKK-----VHVK 361

Db 1103 SVALVKETWVVISPPC-TGSSEHKKPELEBEKILALEKEKEQOLQKQBALTSKAILKKAQ 1161

QY 362 KPSQL--SLGGO-----RCVGFGLDE-----ELAGAFFFIRNAVLGKOPNRTTA 405

Db 1162 EKERHLREBLQKQDQYNNLQEOFDEDSKENEENIGDOLRQLOQVRSIDG-KLPSIDQ 1220

QY 406 ERSST 411

Db 1221 EGSST 1226

RESULT 35

A56539 giantin - human

N;Alternate names: macrogolgin

C;Species: *Homo sapiens* (man)

C;Accession: A56539; S37536

R; Seelig, H.P.; Schranz, P.; Schroeter, H.; Wiemann, C.; Griffiths, G.; Renz, M.  
Mol. Cell. Biol. 14, 2564-2576, 1994

A; Title: Molecular genetic analyses of a 376-kilodalton Golgi complex membrane protein

A; Reference number: A5539; MUID:94187728

A; Accession: A5539  
A; Molecule type: mRNA

A; Residues: 1-3259 <SEE>  
A; Cross-references: EMBL:XF5304; NID:9405714; PIDN:CAA53052.1; PID:9405715

C; Species: GDB:GOLGB1; GCP; GCS371  
A; Gen: GDB:GOLGB1  
A; Cross-references: GDB:454958

A; Map position: 3q13.31-3q13.31  
C; Superfamily: gianin  
C; Keywords: coiled coil; Golgi apparatus; transmembrane protein

F; 3238-3254/Domain: transmembrane #status predicted <TMN>

Query Match 7.3%; Score 174.5; DB 1; Length 3259;  
Best Local Similarity 21.1%; Pred. No. 0.39; Mismatches 115; Conservative 80; Indels 169; Gaps 20; Matches 115; Mismatches 174; Mismatches 174; Indels 169; Gaps 20;

Qy 30 HIDLQIOMFE-----TASRTCPOCRIQYGGKIIINKIIFDQAQEEENVLD----- 76  
Db 720 NLQQLIEERKKNAADNNNSAFTAASEERDQQLSYKERSWATERAQYKOLEMLAERQ 779  
Qy 77 -----  
Db 780 RRIDYESQTAHDNLTQECIHSLSIPEAKSKDVKEVQNLDDYQVQFSEQSTLRSQ 839

Qy 104 IDTLR-DTLE--ER---NATVLSQNALNKA-----LSTLKKOMKFLERQDET 149  
Db 840 LQNKESEVELEGAVYRHISSSKVRLSQALSOQLEITKMDQQLLEKKRDRVEIQTIEEK 899

Qy 150 K-----QAREARARLCKNMKTMEQIELLQSQSRSEVEMTRMGV--- 189  
Db 900 DQDQVTEISFSMTKVNQNEEKSLSGLVEKTLBQNLILSRRAKAKKQVEEDEEVNSGL 959

Qy 190 -----GOSAVEQAVCVSLKKEYENLKE-----PKATGELADRKDLVSS 232  
Db 960 KQNDDEMSPAGQTSKEELQHEFQDILKQKNEQRKQLQALINKELQRLRVSREELANL 1019

Qy 233 RSKLT-----  
Db 1020 KDESKEKEIPSETERGEVEBEDKENKEYSEKCVSKCQEIEIYKOTISEKEVELQHIRKD 1079

Qy 257 LQ--SADQEITSRKKSDDPPSMLEPASATNTIVSRYFESAPVEMNPRIHQPPFGD 313  
Db 1080 LEKLAKEQFOQALVKQMQ--TLQDKINQDQILOQETSENAAIIQKITSWNTDASDQ 1136

Qy 314 EIDLNTFDVNTPTQTSQHQCLP----KKLCLERARSPMQNVLK-----VHKVS 361  
Db 1137 SVALVKETVVISPPC-TSSEHHRPELEEKILALEKEREQOLQKLOEALTSRKAIIKRAQ 1195

Qy 362 KPSQSL-SIGGQ---RCVGELEDE-----ELAGAFPIFIRNAVLGQIQPNRTA 405  
Db 1196 EKERHLREELKQKDYNLQEQPDEQSKENENIGDQLRQLQIqvRESIDG-KLPSTDQ 1254

Qy 406 ESRST 411  
Db 1255 ESSST 1260

RESULT 36  
00084 myosin heavy chain, fast skeletal muscle - rabbit (fragment)  
C; Species: Oryctolagus cuniculus (domestic rabbit)  
C; Accession: 07-sep-1990 #sequence\_revision 07-sep-1990 #text\_change 20-Jun-2000  
C; Residues: 1-1203 <HIR>  
R; Maeda, K.; Szakiel, G.; Wittighofer, A.  
Bur, J. Biochem. 167, 97-102, 1987  
A; Title: Characterization of cDNA coding for the complete light meromyosin portion of a  
A; Reference number: S00084; MUID:87304245  
A; Accession: S00084

A; Molecule type: mRNA  
A; Residues: 1-676 <MAE>  
A; Cross-references: EMBL:X05958; NID:91622; PIDN:CAA29391.1; PID:91364242  
A; Note: the sequence from Fig. 5 is inconsistent with that from Fig. 3 in having 561-  
R; Maeda, K.; Roesch, A.; Maeda, Y.; Kalbitzer, H.R.; Wittighofer, A.  
FEBS Lett. 281, 23-26, 1991  
A; Title: Rabbit skeletal muscle myosin. Unfolded carboxyl-terminus and its role in mo-  
A; Reference number: S14807; MUID:91200294  
A; Status: preliminary  
A; Molecule type: protein  
A; Residues: 668-676 <MA2>  
C; Superfamily: myosin heavy chain; myosin motor domain homology  
C; Keywords: actin binding; AMP; coiled coil; muscle; skeletal muscle  
F; 21-676/Domain: light meromyosin <LM>

Query Match 7.3%; Score 174; DB 2; Length 676;  
Best Local Similarity 20.8%; Pred. No. 0.069; Mismatches 80; Conservative 81; Indels 66; Gaps 13; Matches 80; Conservative 81; Mismatches 157; Indels 66; Gaps 13;

Qy 68 QEBNVLDLAEFLRNELDQWKA-----QLSQD---REKRSQAI---IDLRL 109  
Db 3 KEEH---OLNLNLSSQKARLHTESGEFSRDLQDEKMSLQSGQAFQOIEELKR 58

Qy 110 TLEERNATVESLQNALNFKEMLQSTLKKQMKFLQDQDETKOREEAH----RLKCKM 163  
Db 59 QLEBETKAKSALAHALQSSRRDQDLRQYEEBQEARAKLQRQMSKANSEQSOWRTKET 118

Qy 164 KTMQIELLILQSQSRSEVEMTRMGV----- 223  
Db 119 DAIORTE-ELEAKKKLQARLQD---AEEHVEAVNSKCAASLERTKQRL---NEADLMID 172

Qy 224 RLKKDVLSSRSKLTNE-----LDQAKLELSAQDOSADEITSLRKKDDP 274  
Db 173 VERNATCARMKDKKRNIDKVLAEWKHYEEAOELASQKRSLSTEVERKYNATES 232

Qy 275 PGNLPEASINETVSLVYFESAPVEMNPRLHQ--PPFGDEIDLNTTFDNNTPPTQTSG 333  
Db 233 LDHETLKRKNQHQESDLTQIAESAKHIELEKKKQID----- 275

Qy 334 QHCLPKKKLCLERARSPMQNVLKVKVHKVSPESOLSLGGCQRCVGLDELALAGAFLPFTRNA 393  
Db 276 QKSELQAALEEARGSLEHEEGLRILQELLNQVKSEIDRKLAEDP----DQLKRNH 331

Qy 394 V-LQOKQPRTTAESRSSDVRI 416  
Db 332 LRVYEMSTQDDEBIRSRNDALI 355

RESULT 37  
B55094 chromosomal protein XCAP-E - African clawed frog  
C; Species: Xenopus laevis (African clawed frog)  
C; Date: 23-Mar-1995 #sequence\_revision 05-Apr-1995 #text\_change 02-Jun-2000  
C; Accession: B55094  
R; Hirano, T.; Mitchison, T.J.  
Cell 79, 449-458, 1994  
A; Title: A heterodimeric coiled-coil protein required for mitotic chromosome condensa-  
A; Reference number: A55094; MUID:9504242  
A; Accession: B55094  
A; Status: preliminary  
A; Molecule type: mRNA  
A; Residues: 1-1203 <HIR>  
A; Cross-references: GB:U13674; NID:9563813; PIDN:AAA64680.1; PID:9563814  
C; Species: chromosomal protein SMC1  
C; Keywords: chromosomal protein; DNA condensation; heterodimer

Query Match 7.3%; Score 173.5; DB 2; Length 1203;  
Best Local Similarity 21.9%; Pred. No. 0.14; Mismatches 135; Indels 57; Gaps 11; Matches 73; Conservative 69; Mismatches 135; Indels 57; Gaps 11;

QY	77 EFLKIEELDSYKAQSLQDKREKRDSDQAIIDTDLTDEERNATVESQNALKAEMCSTIK 136
QY	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Db	721 EMKSBEEELQQTQLOQSYHQQEE--LDSIKQTEESLTKTKEVORKAEEFKVLE 778
Qy	137 KOMKMLE-ORQDETKQARE------EHLRKCKMKMWEQIELLQLQSORSEYEMIRD 186
Qy	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Db	779 HMKMKAEAREERELKEAQOKLDTAAKKKAQDAASNNKKEKEQQEVDALV-ELFLKRE 833
Qy	187 MGVGOSAVEQLAVCVSLKKEYENIKEARKATGELADRKKDVLSSRSKLTNLTEQDA 246
Db	834 Q-----TTYKQIETDEAMKAYQEOADSMASEVSKNEAKVKAQDAELAQ 879
Qy	247 KLEIRSAQDQLOSAQDQETLRSKEDDPGPNLERSATNETVSRUVFEDPAPY-EMMP- 304
Db	880 KEIINGHDKEIKTTSSEAGKLRENNNDLQKIKELEHNNSKKKDSADAQAVKMLNDY 939
Qy	305 --RLHQPPGDEIDLNTFDVNTPPTQTSQSQ HCLPLKL-----CLERAR 347
Qy	:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
Db	940 EWIASEKHFHG--QANTAYDFKTNPKAGORLHKLQERKEKEKLGRRNNRARMNLQAE 996
Qy	348 SPMQNVLKVHKVSKPESQISLGGORCVGELDEE 381
Db	997 ERYNDLMMKKRIVENDKSKI---LTIEELDQK 1026
RESULT	38
A48467	myosin heavy chain - nematode (Brugia malayi) (fragment)
C;Species:	Brugia malayi
C;Date:	01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 13-Feb-1998
C;Accession:	A48467
R;Dissanyake, S.; Xu, M.; Plessens, W.F.	
Mol. Biochem. Parasitol. 56, 349-51, 1992	
A;Title:	Myosin heavy chain is a dominant parasite antigen recognized by antibodies in s
A;Reference number:	A48467; MUID:9313325
A;Accession:	A48467
A;Status:	preliminary
A;Molecule type:	nucleic acid
A;Residues:	1-1313 <DIS>
A;Note:	sequence extracted from NCBI backbone (NCBIP:122784, NCBIP:122786)
C;Superfamily:	myosin heavy chain; myosin motor domain homology
C;Keywords:	ATP
Query Match	7.2%; Score 172.5; DB 2; Length 1313;
Best Local Similarity	22.8%; Pred. No. 0.18; Length 1313;
Matches	91; Conservative 57; Mismatches 184; Indels 67; Gaps 13;
Qy	66 LAQEEENVDAEFLKNEQLSYKAQSLQKRE-----KRDSDQAIIDTDLTDEERNATV 118
Db	244 LLEERNNNVE-----NELEAAQAKQSLSDVDRNLRLSTLTKDVEQIHEELERLGQDQDRT 297
Qy	119 ESIQNALWKAEMCSTLKKQMKEL-ORQDETKQAREFAHR-LKCKKTMWEQIELLQ 174
Db	298 SDLRSRKKKTENDVNLKKIAIDLEIRLQTDAAQKSRQIQLQDENQQDENTAKLN 357
Qy	175 SQSEVEENVIRDMCVGQSAVEQLAVCVSLKKE-----NLKEARKATGELADR 226
Db	358 KERKHOEENRKLMDQEEKDGNYSNKLKGKLEQSLDDLENERKGRNPIEKOR 417
Qy	227 KDLVSSRSKLTN-TEPQAKLERSACKDLSQADQETSLRKSDDPGPNLERSAT 285
Db	418 K--IGGELKVAQENMEERORRHEIESNLKKKSEAAQATITRLEEQDLVGLK--KQV 473
Qy	286 ETWSRLV-----FESPAVEMNPRLQHPP-FGDEIDLNTFDVNTPPTQTSQSQ 334
Db	474 ETONRTELEELNERGSRSKADRSQDLOREBEPGIRLDEBGGATAAQVEVNKKRRA 533
Qy	335 HCLPKKLCLIERPSMQL-----KVKHVSPEQISLGGR 373
Db	534 ELAKLRRDLEANNHNEQOLAAIRKNDAAVAELDQIEAQAKRKIEKDQIAQDDED 593
RESULT	39
138055	myosin heavy chain, perinatal skeletal muscle - human
N;Contains:	myosin ATPase (EC 3.6.1.32)
C;Species:	Homo sapiens (man)
C;Date:	17-May-1996 #sequence_revision 17-May-1996 #text_change 02-Feb-2001
C;Accession:	I38055; MUID:10154; S12459; S09332; A30220; S9478
R;Julian, E.H.; Kelly, A.M.; Pompidou, A.J.; Hoffman, R.; Schiaffino, S.; Stedman, P.	
Eur. J. Biochem. 230, 1001-1006, 1995	
A;Title:	Characterization of a human perinatal myosin heavy-chain transcript.
A;Reference number:	I38055; MUID:9324556
A;Accession:	I38055
A;Status:	translated from GB/EMBL/DDBJ
A;Molecule type:	mRNA
A;Residues:	1-1937 <RES>
A;Cross-references:	EMBL:238133; NID:9558668; PIDN:CAA6293; PID:9558669
R;Karsch-Mirachini, I.; Peghalal, R.; Shows, T.B.; Leinwand, L.A.	
Gene 89, 289-294, 1990	
A;Title:	Generation of a full-length human perinatal myosin heavy-chain-encoding cDNA
A;Reference number:	JH0154; MUID:90323631
A;Accession:	JH0154
A;Molecule type:	mRNA
A;Residues:	1-14, 'A', 16-859 <KAR>
A;Cross-references:	GB:Y00821
A;Experimental source:	skeletal muscle
R;Bober, E.	
A;Submitted to the EMBL Data Library, January 1989	
A;Reference number:	S12458
A;Accession:	S12459
A;Molecule type:	mRNA
A;Residues:	502-1071, 'N' 1073-1250, 'DGG' 1253-1376, 'NT' 1379-1913, 'D' 1915-1937 <BOB>
A;Cross-references:	EMBL:X51592; NID:929465; PIDN:CAA35941.1; PID:929466
A;Experimental source:	clone GTMHC-F
R;Bober, E.; Buchberger-Heidl, A.; Braun, T.; Singh, S.; Goedde, H.W.; Arnold, H.H.	
Eur. J. Biochem. 189, 55-65, 1990	
A;Title:	Identification of three developmentally controlled isoforms of human myosin
A;Reference number:	S09331; MUID:90235862
A;Accession:	S09332
A;Molecule type:	mRNA
A;Residues:	860-969, 'Q' 971-1246, 'H' 1248-1280, 'G' 1262-1296, 'Q' 1298-1503, 'AH' 1506-1736, 'NT' 1379-1386, 'X' 1388-1456, 'X' 1458-1526, 'X' 1528-1596, 'X' 1598-1666, 'X' 1666-1736
A;Cross-references:	EMBL:X51592
R;Feghali, R.; Leinwand, L.A.	
J. Cell Biol. 108, 1791-1797, 1989	
A;Title:	Molecular genetic characterization of a developmentally regulated human per
A;Reference number:	A30220; MUID:89234168
A;Accession:	A30220
A;Status:	preliminary
A;Molecule type:	mRNA
A;Residues:	860-969, 'Q' 971-1246, 'H' 1248-1280, 'G' 1262-1296, 'Q' 1298-1503, 'AH' 1506-1736, 'NT' 1379-1386, 'X' 1388-1456, 'X' 1458-1526, 'X' 1528-1596, 'X' 1598-1666, 'X' 1666-1736
C;Genetics:	
A;Gene:	GDB:MYH8
A;Cross-references:	GDB:125267; OMIM:160741
A;Map position:	17pter-17p12
C;Superfamily:	myosin heavy chain; myosin motor domain homology
C;Keywords:	actin binding; ATP; coiled coil; hydrolase; muscle contraction; nucleotide binding; myosin motor domain homology <MM02>
F;19-769;/domain:	myosin motor domain homology
F;181-188;/Region:	nucleotide-binding motif A (P-loop)
F;551-588;/Region:	actin binding #status predicted
F;650-680;/Region:	actin binding #status predicted
F;844-1282;/Region:	F844-1282;Region: S2 #status predicted
F;698,708;/Active site:	Cys #status predicted
Query Match	7.2%; Score 172.5; DB 2; Length 1937;
Best Local Similarity	19.8%; Pred. No. 0.27;

QY	55	KRTINKLFLDQASERBENVDAEFLKNEELLSVYKAQSLQSQKIREKRSQAITDLRTLEER
Db	1269	QORLINDL--TAQRARLQTEAGEYRSQLDKDALVLSQSLRSQASTQQIEELKHOLEEP
Qy	115	NATVESLQNLANKAEMCSTLKKQMFLEQRQDETKQAREHARLKKMKTMEQIELLO
Db	1326	TKAKNALAHALQSSRHDCLLREQEEQGKQALRQASANKELETKQRLQNEVEDLMDVERSNAAC
QY	175	SORSEVEE---MIRDVGQOSAVEQLAVYCUSLKVKEYENLK-----ERKATGE
Db	1386	TE-ELEAKKKLQRLQEEAHVAVNAVKASLEKTQRLQNEVEDLMDVERSNAAC
QY	221	LADRKK--ILVSSRSKLKLNTEDOAKELRSLRQDQSADEITSRKKSDPQGNL
Db	1444	ALDKKQNRFDKVLSEWKQK----YEETQAELEASQESRSLSTLFKVKNVYESLDL
Qy	279	EPASATNETTSRLVESPAPVEMMPRLHOPPFGEDEIDLNTFDVNTPPTQTSQSHQCLP
Db	1499	ETLRENRKNQFQESLDLTDQIAEGKQH-----LEKKKQVEKE
QY	339	KKLCLEBRASPQMVNLKVKVSKPESOLSLGGORCVGELDEELAGAPFLFIRNALVGK
Db	1543	IQAALSEEAERASLEHEBGKIRIQLINQVSEVDRKIAERDE-----IDQL
QY	399	QPNRT-----TAESSTDWVRI
Db	1590	KRNHTRVETVNTQSTLDAEIRSRNDALRV
A:Note: F5E19_70		
RESULT 40		
T51505		
hypothetical protein F5E19_70 - <i>Arabidopsis thaliana</i>		
C;Species: <i>Arabidopsis thaliana</i> (mouse-ear cress)		
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000		
C;Accession: T51505		
R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tazawa, A.; Reference number: 225394		
A;Accession: T51505		
A;Status: preliminary		
A;Molecule type: DNA		
A;Residues: 1-853 <AT>		
A;Cross references: EMBL:AL391147		
A;Experimental source: cultivar Columbia; BAC clone F5E19		
A;Genetics:		
A;Map position: 5		
A;Introns: 6/2; 79/3		
A;Note: F5E19_70		
Query Match 7.2%; Score 171.5; DB 2; Length 853;		
Best Local Similarity 19.7%; Pred. 0.12; Mismatches 92; Gaps 82; Conservative 92; Indels 95; Gaps 82; Matches 148; Gaps 82;		
Qy	66	LAQEERNLVDAEFLKNELDQKAQSLQKDRQSQDQASQITDPLDTEERAVATVESLQNL
Db	382	VAKQRE--DLEVSFQRIGSVEEVDKNEKEVKLSEETVK--EEKRNALKQEDAT
Qy	126	NKAEMCSTLKKQMFLE--QDQETKORE-----EAHRLKKMKT-----
Db	436	SRVORLSEEKSKLSDLESSKREEEKSQKAMESLASALHVSVSSEGRELKKLQLSGQDHEY
Qy	166	--MEDIUILLQSQSEVEEMI---RDMVGQOSAVEQLAVYCUSLKVKEYENLKEAR--
Db	496	ETQDIDDLKVIKATNEKYENLDEARHETQYLVLSAVEQTLVFSQPKKHESSKQDE-MKEANLYN
Qy	216	-----KATGELADRLKDLVSLRSKSLTNTS-----LQD
Db	555	YVKKMEEDVASMGMKGEMNRDLNLKKRTEEDAAWKKEAQTKDSLKEVEEFTIVYLOETLG
Qy	246	AKLELRSAQQLQSLQADQETTSRKSSDPPGPNLEASATNETVSLVLFESQPKVEMMPR

Search completed: September 4, 2002, 16:12:55  
Job time: 3239 sec

Qy	306	LHQPPGCDDEIOLNTTDVNTPTQTSQHQLPK - KLCLEARARSPMQNLLKKVHV - S	361
Db	670	OPEENGELSEKDYDL - - - - - LPKVVFSESSHRSVEEKSAVTPLDHE	716
Qy	362	KPESQSLGGQRVGELDELAGAFLFIRAVLGKQPNRTAESA RSSDVWRIGF	418
Db	717	PPQEIQNSNGNSNGMEEKEVNG - - - - - KPEVETTEKKEDESODDDKIDSVEVIF	767

